

Amendments to the Specification:

Please amend the specification as shown:

Please delete the paragraphs [0046] through [0048] and replace them with the following paragraphs:

[0046] RNA was prepared from the cells after 3 days in culture and is used to construct a cDNA library in the vector λ gt10. This cDNA library was screened using a ^{32}P -labeled degenerate oligonucleotide probe containing all possible permutations coding for the sequence of amino acids, HTGEKP (SEQ ID NO: 6).

[0047] The HTGEKP (SEQ ID NO: 6) sequence is a sequence motif common to proteins of the class called “zinc-finger” proteins. Such zinc-finger proteins have the ability to bind to DNA and these proteins have been shown to be transcription factors. Zinc-finger transcription factors of the Cys₂His₂ type are characterized by tandem arrays of sequence conforming approximately to the motif (Tyr, Phe)-X-Cys-X₂₄-Cys-X₃-Phe-X₅-Leu-X₂-His-X₃₋₅-His (SEQ ID NO: 7), where X represents any essential amino acid. The linker that connects adjacent zinc-finger domains is well conserved and has the consensus sequence His-Thr-Gly-Glu-Lys-Pro (HTGEKP) (SEQ ID NO: 6). Therefore, a degenerate oligonucleotide probe representative of all possible codons encoding HTGEKP (SEQ ID NO: 6) will hybridize to cDNA clones within the library encoding zinc-finger motifs.

[0048] Approximately 60,000 λ plaques were screened and plaques hybridizing to the degenerate HTGEKP (SEQ ID NO: 6) probe were obtained. The cDNA inserts of these hybridizing clones were amplified using the polymerase chain reaction (PCR), cloned by the TA-tailing method, and the DNA sequence of the inserts was obtained. The obtained DNA sequences were compared to the NCBI nucleotide sequence database using the BLAST algorithm. The BLAST search showed that the one of the inserts (called CZF-1; Cartilage Zinc Finger) matched a 717 amino acid open reading frame (ORF) encoding a protein containing approximately 16 zinc-finger domains, within a 3.6 Mb region in 19q13.4. Additional sequence encoding the amino acid terminal region of the protein is obtained by performing a 5' RACE procedure. The final protein sequence was found to be 717 amino acid residues in length.

Appl. No. 10/623,914
Amdt. dated March 16, 2007
Response to Office Action of October 18, 2007.

Please delete the paragraph [0102] and replace it with the following paragraph:

[0102] RNA was prepared from the cells of Example 1 that had been in culture for 3 days, and used to construct a cDNA library in the λ gt10 vector using standard methods well known to those in the art. This library was screened, using a 32 P-labeled degenerate oligonucleotide probe, coding for the HTGEKP (SEQ ID NO: 6) sequence (5'-CA(CT)AC(ACTG) GG(ACTG) GA(AG) AA(AG) CC(ATCG)-3', SEQ ID NO. 5). Cloned cDNA inserts from λ gt10 clones that hybridized to the oligonucleotide probe were amplified from hybridizing plaques by PCR using LD insert screening amplimers (Clontech) as primers. Inserts were cloned directly into the pCR[®]2.1 plasmid vector (Invitrogen).

Please amend paragraph [119] of the application as follows:

[0119] The DNA sequences were analyzed using the BLASTX program at NCBI (~~http://www.ncbi.nlm.nih.gov/~~). All databases including dbEST, dbSTS, and the non-redundant database were searched.

Please replace Figure 3 and Figure 5 of the application with the attached Figures 3 and 5.

Please replace the sequence listing with the sequence listing that is attached hereto.